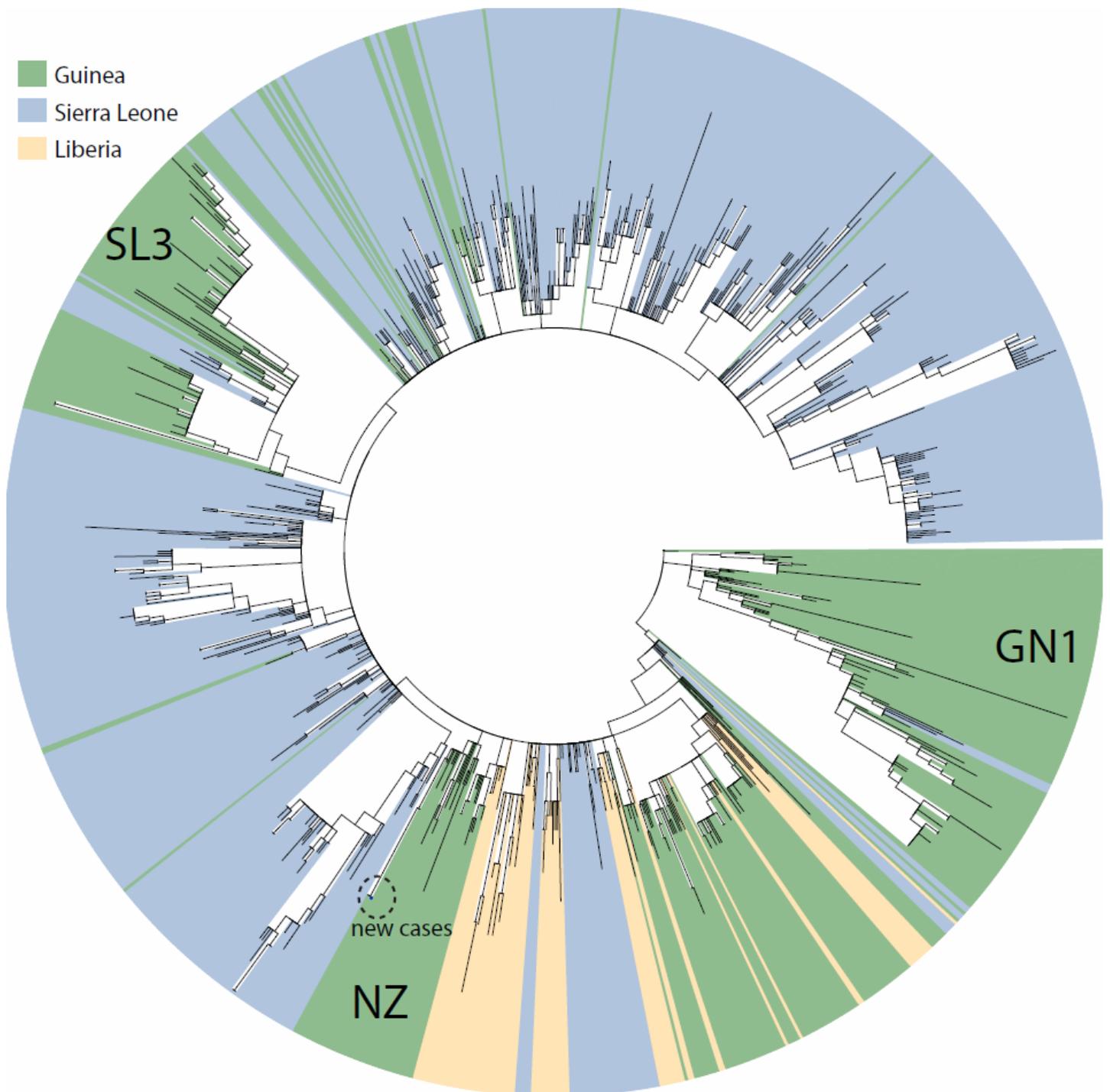


**Figure S1. Complete maximum-likelihood phylogenetic tree of 1,066 historical Ebola genome sequences and the new cases described here.** Phylogenetic reconstruction was performed by maximum likelihood under the GTR+Gamma model using RAxML [4]. The GN1 and SL3 lineages were the only lineages detected during surveillance sequencing of EVD cases in Guinea during the second half of 2015. The new cases (location depicted by circle) belong to a different cluster termed NZ that was last observed in 2014. The tree is colour coded according to the country of origin of each genome sequence.



**Figure S2. Root-to-tip analysis.** Root-to-tip regression analysis for 1,066 Ebola virus genomes collected during the outbreak including the new sequences was performed with program TempEst [5]. The yellow dot represents the survivor's acute sample from November 2014. The red dot represents the survivor's semen sample collected 504 days later in March 2016. The virus in both samples differed by five novel mutations (Table S1), which equates to an evolutionary rate of  $0.19 \times 10^{-3}$  substitutions per site per year.

